

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : David White et al.  
Serial No.: 09/195,896  
Filed : November 19, 1998  
Title : LEPTIN INDUCED GENES

Art Unit:  
Examiner:

Box Sequence  
Assistant Commissioner for Patents  
Washington, DC 20231

VERIFIED STATEMENT UNDER 37 CFR § 1.821 (f)

I, Maureen Ruttle, declare that I personally prepared the paper and the computer-readable copies of the Sequence Listing filed herewith in the above-entitled case and that the content of both is the same.

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of The United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Date: Nov 15, 1999

Maureen Ruttle  
Maureen Ruttle

Fish & Richardson P.C.  
225 Franklin Street  
Boston, MA 02110-2804

Telephone: 617/542-5070  
Facsimile: 617/542-8906

Date of Deposit November 29, 1999  
I hereby certify under 37 CFR 1.8(a) that this correspondence is being deposited with the United States Postal Service as **first class mail** with sufficient postage on the date indicated above and is addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231.

Carrie A. Amonte

## SEQUENCE LISTING

<110> White, David  
Zhou, Jianghong  
Tartaglia, Louis A.

<120> LEPTIN INDUCED GENES

<130> 07334/109001

<140> US 09/195,896

<141> 1998-11-19

<150> US 60/108,379

<151> 1998-10-29

<150> US 09/150,857

<151> 1998-09-10

<160> 17

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1196

<212> DNA

<213> Mus musculus

<400> 1

agatgagtgt	ggggcgctcga	agagtcaagt	tgctgggcat	cctgatgatg	gcaaagtgtct	60
tcattttattt	gattgtggaa	gtctccaaaa	acagtagcca	agacaaaaat	ggaaagggag	120
gagtaataat	cccgaaagag	aagttctgga	agccaccag	cactccccgg	gcatactgga	180
acagggaaca	ggagaagctg	aacagggtgt	acaatcccat	cttgaacagg	gtggccaatc	240
agacagggga	gctagccaca	tctccaaaca	caagtcacct	gagctattgt	gaaccagact	300
cgacgggtcat	gacagctgtg	acagatttta	ataatctgcc	ggacagattt	aaagactttc	360
tcttgtattt	gagatgccgg	aattactcgc	tgcttataga	tcaaccgaag	aaatgtgcaa	420
agaagccctt	cttactattg	gcgataaagt	ccctcattcc	acattttgcc	agaaggcaag	480
caattcggga	gtcttggggc	cgagaaacca	acgtagggaa	ccagacagta	gtgagggctt	540
tcctgttggg	caagacaccc	ccagaggaca	accaccctga	cctttcggac	atgcttaagt	600
ttgagagtga	caagcaccag	gacatcctca	tgtggaacta	tagagacaca	ttcttcaacc	660
tgtccctgaa	ggaagtgtctg	tttcttaggt	gggtgagcac	ttcctgtcca	gacgcagagt	720
ttgtcttcaa	gggcgatgat	gacgtgtttg	tgaacaccca	tcacatcctt	aattacttga	780
atagcttatc	caagagcaaa	gccaaagact	tgttcatagg	tgacgtgatc	cacaatgctg	840
ggcctcaccg	ggataagaaa	ctgaagtact	acatcccaga	agtcttctac	accggcgtct	900
acccaccgta	tgccgggggt	ggtggattcc	tgtactccgg	cccccttgcc	ttgaggctgt	960
acagtgcgac	tagccgggtc	catctctacc	ctattgatga	tgtttatacg	ggaatgtgcc	1020
ttcagaaact	gggccttggt	ccagagaagc	acaaaggctt	caggacattt	gatattgaag	1080
agaaaaataa	gaaaaatatt	tgttcctata	tagacctaat	gttagtacat	agcagaaaac	1140
ctcaagagat	gattgatatc	tggtctcagt	tgcaaagtcc	taatttaaaa	tgctga	1196

<210> 2

<211> 397

<212> PRT

<213> Mus musculus

<400> 2

Met	Ser	Val	Gly	Arg	Arg	Arg	Val	Lys	Leu	Leu	Gly	Ile	Leu	Met	Met
1				5				10					15		
Ala	Asn	Val	Phe	Ile	Tyr	Leu	Ile	Val	Glu	Val	Ser	Lys	Asn	Ser	Ser
			20					25					30		

Gln Asp Lys Asn Gly Lys Gly Gly Val Ile Ile Pro Lys Glu Lys Phe  
           35                          40                          45  
 Trp Lys Pro Pro Ser Thr Pro Arg Ala Tyr Trp Asn Arg Glu Gln Glu  
       50                          55                          60  
 Lys Leu Asn Arg Trp Tyr Asn Pro Ile Leu Asn Arg Val Ala Asn Gln  
       65                          70                          75                          80  
 Thr Gly Glu Leu Ala Thr Ser Pro Asn Thr Ser His Leu Ser Tyr Cys  
                           85                          90                          95  
 Glu Pro Asp Ser Thr Val Met Thr Ala Val Thr Asp Phe Asn Asn Leu  
                           100                          105                          110  
 Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn Tyr  
                           115                          120                          125  
 Ser Leu Leu Ile Asp Gln Pro Lys Lys Cys Ala Lys Lys Pro Phe Leu  
       130                          135                          140  
 Leu Leu Ala Ile Lys Ser Leu Ile Pro His Phe Ala Arg Arg Gln Ala  
       145                          150                          155                          160  
 Ile Arg Glu Ser Trp Gly Arg Glu Thr Asn Val Gly Asn Gln Thr Val  
                           165                          170                          175  
 Val Arg Val Phe Leu Leu Gly Lys Thr Pro Pro Glu Asp Asn His Pro  
                           180                          185                          190  
 Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Asp Lys His Gln Asp Ile  
                           195                          200                          205  
 Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys Glu  
       210                          215                          220  
 Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Ala Glu Phe  
       225                          230                          235                          240  
 Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile Leu  
                           245                          250                          255  
 Asn Tyr Leu Asn Ser Leu Ser Lys Ser Lys Ala Lys Asp Leu Phe Ile  
                           260                          265                          270  
 Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys  
       275                          280                          285  
 Tyr Tyr Ile Pro Glu Val Phe Tyr Thr Gly Val Tyr Pro Pro Tyr Ala  
       290                          295                          300  
 Gly Gly Gly Gly Phe Leu Tyr Ser Gly Pro Ala Leu Leu Arg Leu Tyr  
       305                          310                          315                          320  
 Ser Ala Thr Ser Arg Val His Leu Tyr Pro Ile Asp Asp Val Tyr Thr  
                           325                          330                          335  
 Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys Gly  
                           340                          345                          350  
 Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Lys Asn Ile Cys Ser  
                           355                          360                          365  
 Tyr Ile Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met Ile  
       370                          375                          380  
 Asp Ile Trp Ser Gln Leu Gln Ser Pro Asn Leu Lys Cys  
       385                          390                          395

<210> 3  
 <211> 1191  
 <212> DNA  
 <213> Mus musculus

<400> 3  
 atgagtgttg ggcgtcgaag agtcaagttg ctgggcatcc tgatgatggc aaatgtcttc 60  
 atttatttga ttgtggaagt ctccaaaaac agtagccaag acaaaaatgg aaagggaggga 120  
 gtaataatcc cgaaagagaa gttctggaag ccacccagca ctccccgggc atactggaac 180  
 agggaaacagg agaagctgaa caggtggtac aatcccattc tgaacagggt ggccaatcag 240  
 acagggggagc tagccacatc tccaaacaca agtcacctga gctattgtga accagactcg 300  
 acggctcatga cagctgtgac agatttttaaat aatctgccgg acagattttaa agactttctc 360  
 ttgtatttga gatgccggaa ttactcgtg cttatagatc aaccgaagaa atgtgcaaag 420  
 aagcccttct tactattggc gataaagtcc ctcattccac attttgccag aaggcaagca 480  
 attcgggagat cttgggggccc agaaaccaac gtagggaacc agacagtagt gaggggtcttc 540

```
<210> 4
<211> 365
<212> PRT
<213> Mus musculus
```

<400> 4															
Gln 1	Asp	Lys	Asn	Gly 5	Lys	Gly	Gly	Val	Ile 10	Ile	Pro	Lys	Glu	Lys 15	Phe
Trp	Lys	Pro	Pro 20	Ser	Thr	Pro	Arg	Ala 25	Tyr	Trp	Asn	Arg	Glu 30	Gln	Glu
Lys	Leu	Asn 35	Arg	Trp	Tyr	Asn 40	Pro	Ile	Leu	Asn	Arg 45	Val	Ala	Asn	Gln
Thr 50	Gly	Glu	Leu	Ala	Thr	Ser 55	Pro	Asn	Thr	Ser	His 60	Leu	Ser	Tyr	Cys
Glu 65	Pro	Asp	Ser	Thr	Val 70	Met	Thr	Ala	Val	Thr 75	Asp	Phe	Asn	Asn	Leu 80
Pro	Asp	Arg	Phe	Lys 85	Asp	Phe	Leu	Leu	Tyr 90	Leu	Arg	Cys	Arg	Asn 95	Tyr
Ser	Leu	Leu	Ile 100	Asp	Gln	Pro	Lys	Lys 105	Cys	Ala	Lys	Lys	Pro 110	Phe	Leu
Leu	Leu	Ala 115	Ile	Lys	Ser	Leu	Ile 120	Pro	His	Phe	Ala	Arg 125	Arg	Gln	Ala
Ile 130	Arg	Glu	Ser	Trp	Gly 135	Arg	Glu	Thr	Asn	Val	Gly 140	Asn	Gln	Thr	Val
Val 145	Arg	Val	Phe	Leu	Leu 150	Gly	Lys	Thr	Pro	Pro 155	Glu	Asp	Asn	His	Pro 160
Asp	Leu	Ser	Asp	Met 165	Leu	Lys	Phe	Glu	Ser 170	Asp	Lys	His	Gln	Asp 175	Ile
Leu	Met	Trp	Asn 180	Tyr	Arg	Asp	Thr	Phe 185	Phe	Asn	Leu	Ser	Leu 190	Lys	Glu
Val	Leu	Phe 195	Leu	Arg	Trp	Val	Ser 200	Thr	Ser	Cys	Pro	Asp 205	Ala	Glu	Phe
Val 210	Phe	Lys	Gly	Asp	Asp	Asp 215	Val	Phe	Val	Asn	Thr 220	His	His	Ile	Leu
Asn 225	Tyr	Leu	Asn	Ser	Leu 230	Ser	Lys	Ser	Lys	Ala 235	Lys	Asp	Leu	Phe	Ile 240
Gly	Asp	Val	Ile	His 245	Asn	Ala	Gly	Pro	His 250	Arg	Asp	Lys	Lys	Leu 255	Lys
Tyr	Tyr	Ile	Pro 260	Glu	Val	Phe	Tyr	Thr 265	Gly	Val	Tyr	Pro	Pro 270	Tyr	Ala
Gly	Gly	Gly 275	Gly	Phe	Leu	Tyr	Ser 280	Gly	Pro	Ala	Leu	Leu 285	Arg	Leu	Tyr
Ser	Ala	Thr	Ser	Arg	Val	His 295	Leu	Tyr	Pro	Ile	Asp 300	Asp	Val	Tyr	Thr
Gly 305	Met	Cys	Leu	Gln	Lys 310	Leu	Gly	Leu	Val	Pro 315	Glu	Lys	His	Lys	Gly 320
Phe	Arg	Thr	Phe	Asp 325	Ile	Glu	Glu	Lys	Asn 330	Lys	Lys	Asn	Ile	Cys 335	Ser
Tyr	Ile	Asp	Leu 340	Met	Leu	Val	His	Ser 345	Arg	Lys	Pro	Gln	Glu 350	Met	Ile

Asp Ile Trp Ser Gln Leu Gln Ser Pro Asn Leu Lys Cys  
 355 360 365

<210> 5  
 <211> 1203  
 <212> DNA  
 <213> Mus musculus

<400> 5  
 atgatttgcc cttcagcttt actggttatt ttaagaaatt taatacggga agaaaaaatc 60  
 atttctcaag agatcctcaa tttgattgaa ttaaggatga aaaaaggga tattcagttg 120  
 acaaaactctg caatcagtga tgcattaaaa gaaatcgata gtagtggtgt caatgttgct 180  
 gtcaccgggg agacgggatc aggggaagtcc agcttcatca ataccctgag aggcattggg 240  
 aatgaagaag aaggtgcagc taaaactggg gtggtggagg taaccatgga aagacatcca 300  
 taaaaacacc ccaatatacc caatgtggtt ttttgggacc tgccctgggat tggaagcaca 360  
 aatttccac caaacactta cctggagaaa atgaagtctt atgagtacga tttcttcatt 420  
 attatttcgg ccacacgctt caagaaaaat gatatagaca ttgccaaagc aatcagcatg 480  
 atgaagaagg aattctactt cgtgagaacc aaggtggact ctgacataac aaatgaagca 540  
 gatggcaaac ctcaaaccct tgacaaagaa aaggtcctgc aggacatccg ccttaactgt 600  
 gtgaacacct ttagggagaa tggcattgct gagccaccaa tcttctgtgt ctctaacaaa 660  
 aatgtttgtc actatgactt ccccgctctg atggacaagc tgataagtga cctccctatc 720  
 tacaggagac acaattttat ggtctcctta cccaatatca cagattcagt cattgaaaag 780  
 aagcggcaat ttctgaagca raggatttgg ctggaaggat ttgctgctga cctagtgaat 840  
 atcatccctt ctctgacctt tctcttggac agtgatttgg agactctgaa gaaaagcatg 900  
 aaattctacc gcactgtgtt tggagtggat gaaacatctt tgcagagatt agctagggac 960  
 tgggaaatag aggtggatca ggtggaggcc atgataaaat ctctgtgtgt gttcaaacct 1020  
 acagatgaag aaacaatata agaaaggctt tcaagatata ttcaggagtt ctgtttggct 1080  
 aatgggtact tacttccctaa aaatagtttt cttaaagaaa tattttacct gaaatattat 1140  
 ttccttgaca tgggtgactga ggatgctaaa actcttctta aagagatatg tttaagaaac 1200  
 tag 1203

<210> 6  
 <211> 400  
 <212> PRT  
 <213> Mus musculus

<400> 6  
 Met Ile Cys Pro Ser Ala Leu Leu Val Ile Leu Arg Asn Leu Ile Arg  
 1 5 10 15  
 Glu Glu Lys Ile Ile Ser Gln Glu Ile Leu Asn Leu Ile Glu Leu Arg  
 20 25 30  
 Met Lys Lys Gly Asn Ile Gln Leu Thr Asn Ser Ala Ile Ser Asp Ala  
 35 40 45  
 Leu Lys Glu Ile Asp Ser Ser Val Leu Asn Val Ala Val Thr Gly Glu  
 50 55 60  
 Thr Gly Ser Gly Lys Ser Phe Ile Asn Thr Leu Arg Gly Ile Gly  
 65 70 75 80  
 Asn Glu Glu Glu Gly Ala Ala Lys Thr Gly Val Val Glu Val Thr Met  
 85 90 95  
 Glu Arg His Pro Tyr Lys His Pro Asn Ile Pro Asn Val Val Phe Trp  
 100 105 110  
 Asp Leu Pro Gly Ile Gly Ser Thr Asn Phe Pro Pro Asn Thr Tyr Leu  
 115 120 125  
 Glu Lys Met Lys Phe Tyr Glu Tyr Asp Phe Phe Ile Ile Ile Ser Ala  
 130 135 140  
 Thr Arg Phe Lys Lys Asn Asp Ile Asp Ile Ala Lys Ala Ile Ser Met  
 145 150 155 160  
 Met Lys Lys Glu Phe Tyr Phe Val Arg Thr Lys Val Asp Ser Asp Ile  
 165 170 175  
 Thr Asn Glu Ala Asp Gly Lys Pro Gln Thr Phe Asp Lys Glu Lys Val  
 180 185 190

Leu Gln Asp Ile Arg Leu Asn Cys Val Asn Thr Phe Arg Glu Asn Gly  
 195 200 205  
 Ile Ala Glu Pro Pro Ile Phe Leu Leu Ser Asn Lys Asn Val Cys His  
 210 215 220  
 Tyr Asp Phe Pro Val Leu Met Asp Lys Leu Ile Ser Asp Leu Pro Ile  
 225 230 235 240  
 Tyr Arg Arg His Asn Phe Met Val Ser Leu Pro Asn Ile Thr Asp Ser  
 245 250 255  
 Val Ile Glu Lys Lys Arg Gln Phe Leu Lys Gln Arg Ile Trp Leu Glu  
 260 265 270  
 Gly Phe Ala Ala Asp Leu Val Asn Ile Ile Pro Ser Leu Thr Phe Leu  
 275 280 285  
 Leu Asp Ser Asp Leu Glu Thr Leu Lys Lys Ser Met Lys Phe Tyr Arg  
 290 295 300  
 Thr Val Phe Gly Val Asp Glu Thr Ser Leu Gln Arg Leu Ala Arg Asp  
 305 310 315 320  
 Trp Glu Ile Glu Val Asp Gln Val Glu Ala Met Ile Lys Ser Pro Ala  
 325 330 335  
 Val Phe Lys Pro Thr Asp Glu Glu Thr Ile Gln Glu Arg Leu Ser Arg  
 340 345 350  
 Tyr Ile Gln Glu Phe Cys Leu Ala Asn Gly Tyr Leu Leu Pro Lys Asn  
 355 360 365  
 Ser Phe Leu Lys Glu Ile Phe Tyr Leu Lys Tyr Tyr Phe Leu Asp Met  
 370 375 380  
 Val Thr Glu Asp Ala Lys Thr Leu Leu Lys Glu Ile Cys Leu Arg Asn  
 385 390 395 400

<210> 7  
 <211> 1200  
 <212> DNA  
 <213> Mus musculus

<400> 7  
 atgatttgcc cttcagcttt actggttatt ttaagaaatt taatacggga agaaaaaatc 60  
 atttctcaag agatcctcaa tttgattgaa ttaaggatga aaaaaggga tattcagttg 120  
 acaaactctg caatcagtga tgcattaaaa gaaatcgata gtagtgtgct caatggtgct 180  
 gtcaccgggg agacgggatc agggaagtcc agcttcatca ataccctgag aggcatggg 240  
 aatgaagaag aagggtgcagc taaaactggg gtggtggagg taaccatgga aagacatcca 300  
 taaaaacacc ccaatatacc caatgtggtt ttttgggacc tgccctgggat tgggaagcaca 360  
 aatttcccac caaacactta cctggagaaa atgaagtct atgagtacga tttcttcatt 420  
 attatttcgg ccacacgctt caagaaaaat gatatagaca ttgccaaagc aatcagcatg 480  
 atgaagaagg aattctactt cgtgagaacc aagggtggact ctgacataac aaatgaagca 540  
 gatggcaaac ctcaaacctt tgacaaagaa aaggtcctgc aggacatccg ccttaactgt 600  
 gtgaacacct ttagggagaa tggcattgct gagccaccaa tcttcctgct ctctaacaaa 660  
 aatgtttgtc actatgactt ccccgctctg atggacaagc tgataagtga cctccctatc 720  
 tacaggagac acaattttat ggtctcctta cccaatatca cagattcagt cattgaaaag 780  
 aagcggcaat ttctgaagca raggatttgg ctggaaggat ttgctgctga cctagtgaat 840  
 atcatccctt ctctgacctt tctcttgga agtgatttgg agactctgaa gaaaagcatg 900  
 aaattctacc gcactgtggt tggagtggat gaaacatctt tgcagagatt agctagggac 960  
 tgggaaatag aggtggatca ggtggaggcc atgataaaat ctcttgctgt gttcaaacct 1020  
 acagatgaag aaacaatata agaaaggctt tcaagatata ttcaggagtt ctgtttggct 1080  
 aatgggtact tacttcctaa aaatagtttt cttaaagaaa tattttacct gaaatattat 1140  
 ttccttgaca tgggtgactga ggatgctaaa actcttctta aagagatatg tttaagaaac 1200

<210> 8  
 <211> 326  
 <212> PRT  
 <213> Mus musculus

<400> 8  
 Met Ala Ser Lys Val Ser Cys Leu Tyr Val Leu Ser Val Val Cys Trp  
 1 5 10 15

Ala Ser Ala Leu Trp Tyr Leu Ser Ile Thr Arg Pro Thr Ser Ser Tyr  
 20 25 30  
 Thr Gly Ser Lys Pro Phe Ser His Leu Thr Val Ala Arg Lys Asn Phe  
 35 40 45  
 Thr Phe Gly Asn Ile Arg Thr Arg Pro Ile Asn Pro His Ser Phe Glu  
 50 55 60  
 Phe Leu Ile Asn Glu Pro Asn Lys Cys Glu Lys Asn Ile Pro Phe Leu  
 65 70 75 80  
 Val Ile Leu Ile Ser Thr Thr His Lys Glu Phe Asp Ala Arg Gln Ala  
 85 90 95  
 Ile Arg Glu Thr Trp Gly Asp Glu Asn Asn Phe Lys Gly Ile Lys Ile  
 100 105 110  
 Ala Thr Leu Phe Leu Leu Gly Lys Asn Ala Asp Pro Val Leu Asn Gln  
 115 120 125  
 Met Val Glu Gln Glu Ser Gln Ile Phe His Asp Ile Ile Val Glu Asp  
 130 135 140  
 Phe Ile Asp Ser Tyr His Asn Leu Thr Leu Lys Thr Leu Met Gly Met  
 145 150 155 160  
 Arg Trp Val Ala Thr Phe Cys Ser Lys Ala Lys Tyr Val Met Lys Thr  
 165 170 175  
 Asp Ser Asp Ile Phe Val Asn Met Asp Asn Leu Ile Tyr Lys Leu Leu  
 180 185 190  
 Lys Pro Ser Thr Lys Pro Arg Arg Tyr Phe Thr Gly Tyr Val Ile  
 195 200 205  
 Asn Gly Gly Pro Ile Arg Asp Val Arg Ser Lys Trp Tyr Met Pro Arg  
 210 215 220  
 Asp Leu Tyr Pro Asp Ser Asn Tyr Pro Pro Phe Cys Ser Gly Thr Gly  
 225 230 235 240  
 Tyr Ile Phe Ser Ala Asp Val Ala Glu Leu Ile Tyr Lys Thr Ser Leu  
 245 250 255  
 His Thr Arg Leu Leu His Leu Glu Asp Val Tyr Val Gly Leu Cys Leu  
 260 265 270  
 Arg Lys Leu Gly Ile His Pro Phe Gln Asn Ser Gly Phe Asn His Trp  
 275 280 285  
 Lys Met Ala Tyr Ser Leu Cys Arg Tyr Arg Arg Val Ile Thr Val His  
 290 295 300  
 Gln Ile Ser Pro Glu Glu Met His Arg Ile Trp Asn Asp Met Ser Ser  
 305 310 315 320  
 Lys Lys His Leu Arg Cys  
 325

<210> 9  
 <211> 331  
 <212> PRT  
 <213> Mus musculus

<400> 9  
 Met Ala Pro Ala Val Leu Thr Ala Leu Pro Asn Arg Met Ser Leu Arg  
 1 5 10 15  
 Ser Leu Lys Trp Ser Leu Leu Leu Leu Ser Leu Leu Ser Phe Leu Val  
 20 25 30  
 Ile Trp Tyr Leu Ser Leu Pro His Tyr Asn Val Ile Glu Arg Val Asn  
 35 40 45  
 Trp Met Tyr Phe Tyr Glu Tyr Glu Pro Ile Tyr Arg Gln Asp Phe Arg  
 50 55 60  
 Phe Thr Leu Arg Glu His Ser Asn Cys Ser His Gln Asn Pro Phe Leu  
 65 70 75 80  
 Val Ile Leu Val Thr Ser Arg Pro Ser Asp Val Lys Ala Arg Gln Ala  
 85 90 95  
 Ile Arg Val Thr Trp Gly Glu Lys Lys Ser Trp Trp Gly Tyr Glu Val  
 100 105 110

Leu Thr Phe Phe Leu Leu Gly Gln Gln Ala Glu Arg Glu Asp Lys Thr  
 115 120 125  
 Leu Ala Leu Ser Leu Glu Asp Glu His Val Leu Tyr Gly Asp Ile Ile  
 130 135 140  
 Arg Gln Asp Phe Leu Asp Thr Tyr Asn Asn Leu Thr Leu Lys Thr Ile  
 145 150 155 160  
 Met Ala Phe Arg Trp Val Met Glu Phe Cys Pro Asn Ala Lys Tyr Ile  
 165 170 175  
 Met Lys Thr Asp Thr Asp Val Phe Ile Asn Thr Gly Asn Leu Val Lys  
 180 185 190  
 Tyr Leu Leu Asn Leu Asn His Ser Glu Lys Phe Phe Thr Gly Tyr Pro  
 195 200 205  
 Leu Ile Asp Asn Tyr Ser Tyr Arg Gly Phe Phe His Lys Asn His Ile  
 210 215 220  
 Ser Tyr Gln Glu Tyr Pro Phe Lys Val Phe Pro Pro Tyr Cys Ser Gly  
 225 230 235 240  
 Leu Gly Tyr Ile Met Ser Gly Asp Leu Val Pro Arg Val Tyr Glu Met  
 245 250 255  
 Met Ser His Val Lys Pro Ile Lys Phe Glu Asp Val Tyr Val Gly Ile  
 260 265 270  
 Cys Leu Asn Leu Leu Lys Val Asp Ile His Ile Pro Glu Asp Thr Asn  
 275 280 285  
 Leu Phe Phe Leu Tyr Arg Ile His Leu Asp Val Cys Gln Leu Arg Arg  
 290 295 300  
 Val Ile Ala Ala His Gly Phe Ser Ser Lys Glu Ile Ile Thr Phe Trp  
 305 310 315 320  
 Gln Val Met Leu Arg Asn Thr Thr Cys His Tyr  
 325 330

&lt;210&gt; 10

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Drosophilea melonogaster

&lt;400&gt; 10

Met Gln Ser Lys His Arg Lys Leu Leu Leu Arg Cys Leu Leu Val Leu  
 1 5 10 15  
 Pro Leu Ile Leu Leu Val Asp Tyr Cys Gly Leu Leu Thr His Leu His  
 20 25 30  
 Glu Leu Asn Phe Glu Arg His Phe His Tyr Pro Leu Asn Asp Asp Thr  
 35 40 45  
 Gly Ser Gly Ser Ala Ser Ser Gly Leu Asp Lys Phe Ala Tyr Leu Arg  
 50 55 60  
 Val Pro Ser Phe Thr Ala Glu Val Pro Val Asp Gln Pro Ala Arg Leu  
 65 70 75 80  
 Thr Met Leu Ile Lys Ser Ala Val Gly Asn Ser Arg Arg Arg Glu Ala  
 85 90 95  
 Ile Arg Arg Thr Trp Gly Tyr Glu Gly Arg Phe Ser Asp Val His Leu  
 100 105 110  
 Arg Arg Val Phe Leu Leu Gly Thr Ala Glu Asp Ser Glu Lys Asp Val  
 115 120 125  
 Ala Trp Glu Ser Arg Glu His Gly Asp Ile Leu Gln Ala Asp Phe Thr  
 130 135 140  
 Asp Ala Tyr Phe Asn Asn Thr Leu Lys Thr Met Leu Gly Met Arg Trp  
 145 150 155 160  
 Ala Ser Glu Gln Phe Asn Arg Ser Glu Phe Tyr Leu Phe Val Asp Asp  
 165 170 175  
 Asp Tyr Tyr Val Ser Ala Lys Asn Val Leu Lys Phe Leu Gly Arg Gly  
 180 185 190  
 Arg Gln Ser His Gln Pro Glu Leu Leu Phe Ala Gly His Val Phe Gln  
 195 200 205



```
<210> 11
<211> 422
<212> PRT
<213> Homo sapien
```

	<400>	11													
Met 1	Leu	Gln	Trp	Arg 5	Arg	Arg	His	Cys	Cys 10	Phe	Ala	Lys	Met	Thr 15	Trp
Asn	Ala	Lys	Arg	Ser	Leu	Phe	Arg	Thr	His	Leu	Ile	Gly	Val	Leu	Ser
Leu	Val	Phe	Leu	Phe	Ala	Met	Phe	Leu	Phe	Phe	Asn	His	His	Asp	Trp
Leu	Pro	Gly	Arg	Ala	Gly	Phe	Lys	Glu	Asn	Pro	Val	Thr	Tyr	Thr	Phe
Arg 65	Gly	Phe	Arg	Ser	Thr	Lys	Ser	Glu	Thr	Asn	His	Ser	Ser	Leu	Arg 80
Asn	Ile	Trp	Lys	Glu	Thr	Val	Pro	Gln	Thr	Leu	Arg	Pro	Gln	Thr	Ala
Thr	Asn	Ser	Asn	Asn	Thr	Asp	Leu	Ser	Pro	Gln	Gly	Val	Thr	Gly	Leu
Glu	Asn	Thr	Leu	Ser	Ala	Asn	Gly	Ser	Ile	Tyr	Asn	Glu	Lys	Gly	Thr
Gly	His	Pro	Asn	Ser	Tyr	His	Phe	Lys	Tyr	Ile	Ile	Asn	Glu	Pro	Glu
Lys 145	Cys	Gln	Glu	Lys	Ser	Pro	Phe	Leu	Ile	Leu	Leu	Ile	Ala	Ala	Glu
Pro	Gly	Gln	Ile	Glu	Ala	Arg	Arg	Ala	Ile	Arg	Gln	Thr	Trp	Gly	Asn
Glu	Ser	Leu	Ala	Pro	Gly	Ile	Gln	Ile	Thr	Arg	Ile	Phe	Leu	Leu	Gly
Leu	Ser	Ile	Lys	Leu	Asn	Gly	Tyr	Leu	Gln	Arg	Ala	Ile	Leu	Glu	Glu
Ser	Arg	Gln	Tyr	His	Asp	Ile	Ile	Gln	Gln	Glu	Tyr	Leu	Asp	Thr	Tyr
Tyr 225	Asn	Leu	Thr	Ile	Lys	Thr	Leu	Met	Gly	Met	Asn	Trp	Val	Ala	Thr
Tyr	Cys	Pro	His	Pro	Tyr	Val	Met	Lys	Thr	Asp	Ser	Asp	Met	Met	Phe
Val	Asn	Thr	Glu	Tyr	Leu	Ile	Asn	Lys	Leu	Leu	Lys	Pro	Asp	Leu	Pro
Pro	Arg	His	Asn	Tyr	Phe	Thr	Gly	Tyr	Leu	Met	Arg	Gly	Tyr	Ala	Pro
Asn	Arg	Asn	Lys	Asp	Ser	Lys	Trp	Tyr	Met	Pro	Pro	Asp	Leu	Tyr	Pro

Ser Glu Arg Tyr Pro Val Phe Cys Ser Gly Thr Gly Tyr Val Phe Ser  
 305 310 315 320  
 Gly Asp Leu Ala Glu Lys Ile Phe Lys Val Ser Leu Gly Ile Arg Arg  
 325 330 335  
 Leu His Leu Glu Asp Val Tyr Val Gly Ile Cys Leu Ala Lys Leu Arg  
 340 345 350  
 Ile Asp Pro Val Pro Pro Pro Asn Glu Phe Val Phe Asn His Trp Arg  
 355 360 365  
 Val Ser Tyr Ser Ser Cys Lys Tyr Ser His Leu Ile Thr Ser His Gln  
 370 375 380  
 Phe Gln Pro Ser Glu Leu Ile Lys Tyr Trp Asn His Leu Gln Gln Asn  
 385 390 395 400  
 Lys His Asn Ala Cys Ala Asn Ala Ala Lys Glu Lys Ala Gly Arg Tyr  
 405 410 415  
 Arg His Arg Lys Leu His  
 420

<210> 12  
 <211> 229  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> VARIANT  
 <222> (1)...(229)  
 <223> Xaa = Any Amino Acid

<400> 12  
 Met Ala Xaa Arg Arg Lys Val Leu Leu Arg Leu Leu Val Leu Ser Leu  
 1 5 10 15  
 Val Xaa Leu Xaa Xaa Xaa Phe Xaa Phe Leu Xaa His Trp Phe Phe Pro  
 20 25 30  
 Ile Trp Tyr Leu Ser Ile Pro Leu Arg Pro Gln Thr Gly Ser Xaa Ser  
 35 40 45  
 Xaa Ser Xaa Xaa Leu Ser His Leu Tyr Asn Thr Val Xaa Arg Xaa Asn  
 50 55 60  
 Xaa Xaa Phe Asn Asn Xaa Xaa Thr Arg Pro Ile Asn Ser Xaa Xaa Phe  
 65 70 75 80  
 Glu Phe Leu Ile Asp Glu Pro Xaa Lys Cys Xaa Lys Lys Pro Phe Leu  
 85 90 95  
 Val Leu Leu Ile Lys Ser Xaa Pro Gly Xaa Phe Xaa Ala Arg Gln Ala  
 100 105 110  
 Ile Arg Glu Thr Trp Gly Xaa Glu Xaa Asn Phe Xaa Gly Ile Xaa Val  
 115 120 125  
 Xaa Arg Val Phe Leu Leu Gly Lys Xaa Ala Glu Xaa Xaa Asp Pro Xaa  
 130 135 140  
 Leu Xaa Xaa Met Val Glu Xaa Glu Ser Arg Xaa His Gly Asp Ile Ile  
 145 150 155 160  
 Gln Gln Asp Phe Leu Asp Thr Tyr Phe Asn Leu Thr Leu Lys Thr Leu  
 165 170 175  
 Met Gly Met Arg Trp Val Ala Thr Phe Cys Pro Xaa Ala Glu Tyr Val  
 180 185 190  
 Met Lys Thr Asp Ser Asp Val Phe Val Asn Thr Xaa Asn Leu Leu Asn  
 195 200 205  
 Lys Leu Leu Lys Pro Ser Leu Ser His Arg Xaa Xaa Leu Phe Thr Gly  
 210 215 220  
 Tyr Val Ile Xaa Gly  
 225

<210> 13  
 <211> 1707  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (246)...(1436)

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1707)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 13

acgcgtccgc gcagcggcag cggcagcagc ggcaacaagt gccggaggct agcagagcca	60
agccggagca gtccctgccg ccgacaccgc cgggccgccc gtccggggcg ccgcgcatgg	120
agcgtgagct gcggcggtcg ccgggctgag ccgcgcggag cggccgggac gtggatgtgg	180
ccgcgatctc ccgcccttgc ccccgccccg ccgagctgga gctgctcccg gacaagatat	240
gagaa atg agt gtt gga cgt cga aga ata aag ttg ttg ggt atc ctg atg	290
Met Ser Val Gly Arg Arg Arg Ile Lys Leu Leu Gly Ile Leu Met	
1 5 10 15	
atg gca aat gtc ttc att tat ttt att atg gaa gtc tcc aaa agc agt	338
Met Ala Asn Val Phe Ile Tyr Phe Ile Met Glu Val Ser Lys Ser Ser	
20 25 30	
agc caa gaa aaa aat gga aaa ggg gaa gta ata ata ccc aaa gag aag	386
Ser Gln Glu Lys Asn Gly Lys Gly Glu Val Ile Ile Pro Lys Glu Lys	
35 40 45	
ttc tgg aag ata tct acc cct ccc gag gca tac tgg aac cga gag caa	434
Phe Trp Lys Ile Ser Thr Pro Pro Glu Ala Tyr Trp Asn Arg Glu Gln	
50 55 60	
gag aag ctg aac cgg cag tac aac ccc atc ctg agc atg ctg acc aac	482
Glu Lys Leu Asn Arg Gln Tyr Asn Pro Ile Leu Ser Met Leu Thr Asn	
65 70 75	
cag acg ggg gag gcg ggc agg ctc tcc aat ata agc cat ctg aac tac	530
Gln Thr Gly Glu Ala Gly Arg Leu Ser Asn Ile Ser His Leu Asn Tyr	
80 85 90 95	
tgc gaa cct gac ctg agg gtc acg tcg gtg gtt acg ggt ttt aac aac	578
Cys Glu Pro Asp Leu Arg Val Thr Ser Val Val Thr Gly Phe Asn Asn	
100 105 110	
ttg ccg gac aga ttt aaa gac ttt ctg ctg tat ttg aga tgc cgc aat	626
Leu Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn	
115 120 125	
tat tca ctg ctt ata gat cag ccg gat aag tgt gca aag aaa cct ttc	674
Tyr Ser Leu Leu Ile Asp Gln Pro Asp Lys Cys Ala Lys Lys Pro Phe	
130 135 140	
ttg ttg ctg gcg att aag tcc ctc act cca cat ttt gcc aga agg caa	722
Leu Leu Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Arg Gln	
145 150 155	
gca atc cgg gaa tcc tgg ggc caa gaa agc aac gca ggg aac caa acg	770
Ala Ile Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln Thr	
160 165 170 175	
gtg gtg cga gtc ttc ctg ctg ggc cag aca ccc cca gag gac aac cac	818
Val Val Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn His	
180 185 190	

ccc gac ctt tca gat atg ctg aaa ttt gag agt gag aag cac caa gac 866  
 Pro Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln Asp  
 195 200 205  
 att ctt atg tgg aac tac aga gac act ttc ttc aac ttg tct ctg aag 914  
 Ile Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys  
 210 215 220  
 gaa gtg ctg ttt ctc agg tgg gta agt act tcc tgc cca gac act gag 962  
 Glu Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu  
 225 230 235  
 ttt gtt ttc aag ggc gat gac gat gtt ttt gtg aac acc cat cac atc 1010  
 Phe Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile  
 240 245 250 255  
 ctg aat tac ttg aat agt tta tcc aag acc aaa gcc aaa gat ctc ttc 1058  
 Leu Asn Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe  
 260 265 270  
 ata ggt gat gtg atc cac aat gct gga cct cat cgg gat aag aag ctg 1106  
 Ile Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu  
 275 280 285  
 aag tac tac atc cca gaa gtt gtt tac tct ggc ctc tac cca ccc tat 1154  
 Lys Tyr Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro Tyr  
 290 295 300  
 gca ggg gga ggg ggg ttc ctc tac tcc ggc cac ctg gcc ctg agg ctg 1202  
 Ala Gly Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg Leu  
 305 310 315  
 tac cat atc act gac cag gtc cat ctc tac ccc att gat gac gtt tat 1250  
 Tyr His Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val Tyr  
 320 325 330 335  
 act gga atg tgc ctt cag aaa ctc ggc ctc gtt cca gag aaa cac aaa 1298  
 Thr Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys  
 340 345 350  
 ggc ttc agg aca ttt gat atc gag gag aaa aac aaa aat aac atc tgc 1346  
 Gly Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile Cys  
 355 360 365  
 tcc tat gta gat ctg atg tta gta cat agt aga aaa cct caa gag atg 1394  
 Ser Tyr Val Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met  
 370 375 380  
 att gat att tgg tct cag ttg cag agt gct cat tta aaa tgc 1436  
 Ile Asp Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys  
 385 390 395  
 taaaatagat acaaaactcaa tttkgsatwg raaggggtwt tttgratwgg ycccatgttg 1496  
 ggggtctcaca ttagagtaat ttctatttna ancatgaaat tgcctttatg agtgataccc 1556  
 atttanggcc tctaancctt catttgnact cacgtgaaga agggaaagcg ggagaaggta 1616  
 atttntttat ggtgaatggc aggatattgg tctgacttac cgntagggga ntttaaaact 1676  
 ggnccctttt gaatctgttt ggatggccct t 1707

&lt;210&gt; 14

&lt;211&gt; 397

<212> PRT  
<213> Homo sapiens

<400> 14  
Met Ser Val Gly Arg Arg Arg Ile Lys Leu Leu Gly Ile Leu Met Met  
1 5 10 15  
Ala Asn Val Phe Ile Tyr Phe Ile Met Glu Val Ser Lys Ser Ser Ser  
20 25 30  
Gln Glu Lys Asn Gly Lys Gly Glu Val Ile Ile Pro Lys Glu Lys Phe  
35 40 45  
Trp Lys Ile Ser Thr Pro Pro Glu Ala Tyr Trp Asn Arg Glu Gln Glu  
50 55 60  
Lys Leu Asn Arg Gln Tyr Asn Pro Ile Leu Ser Met Leu Thr Asn Gln  
65 70 75 80  
Thr Gly Glu Ala Gly Arg Leu Ser Asn Ile Ser His Leu Asn Tyr Cys  
85 90 95  
Glu Pro Asp Leu Arg Val Thr Ser Val Val Thr Gly Phe Asn Asn Leu  
100 105 110  
Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn Tyr  
115 120 125  
Ser Leu Leu Ile Asp Gln Pro Asp Lys Cys Ala Lys Lys Pro Phe Leu  
130 135 140  
Leu Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Arg Gln Ala  
145 150 155 160  
Ile Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln Thr Val  
165 170 175  
Val Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn His Pro  
180 185 190  
Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln Asp Ile  
195 200 205  
Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys Glu  
210 215 220  
Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu Phe  
225 230 235 240  
Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile Leu  
245 250 255  
Asn Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe Ile  
260 265 270  
Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys  
275 280 285  
Tyr Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro Tyr Ala  
290 295 300  
Gly Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg Leu Tyr  
305 310 315 320  
His Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val Tyr Thr  
325 330 335  
Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys Gly  
340 345 350  
Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile Cys Ser  
355 360 365  
Tyr Val Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met Ile  
370 375 380  
Asp Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys  
385 390 395

<210> 15  
<211> 365  
<212> PRT  
<213> Homo sapiens

<400> 15  
 Gln Glu Lys Asn Gly Lys Gly Glu Val Ile Ile Pro Lys Glu Lys Phe  
 1 5 10 15  
 Trp Lys Ile Ser Thr Pro Pro Glu Ala Tyr Trp Asn Arg Glu Gln Glu  
 20 25 30  
 Lys Leu Asn Arg Gln Tyr Asn Pro Ile Leu Ser Met Leu Thr Asn Gln  
 35 40 45  
 Thr Gly Glu Ala Gly Arg Leu Ser Asn Ile Ser His Leu Asn Tyr Cys  
 50 55 60  
 Glu Pro Asp Leu Arg Val Thr Ser Val Val Thr Gly Phe Asn Asn Leu  
 65 70 75 80  
 Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn Tyr  
 85 90 95  
 Ser Leu Leu Ile Asp Gln Pro Asp Lys Cys Ala Lys Lys Pro Phe Leu  
 100 105 110  
 Leu Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Gln Ala  
 115 120 125  
 Ile Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln Thr Val  
 130 135 140  
 Val Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn His Pro  
 145 150 155 160  
 Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln Asp Ile  
 165 170 175  
 Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys Glu  
 180 185 190  
 Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu Phe  
 195 200 205  
 Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile Leu  
 210 215 220  
 Asn Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe Ile  
 225 230 235 240  
 Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys  
 245 250 255  
 Tyr Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro Tyr Ala  
 260 265 270  
 Gly Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg Leu Tyr  
 275 280 285  
 His Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val Tyr Thr  
 290 295 300  
 Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys Gly  
 305 310 315 320  
 Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile Cys Ser  
 325 330 335  
 Tyr Val Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met Ile  
 340 345 350  
 Asp Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys  
 355 360 365

<210> 16

<211> 20

<212> DNA

<213> Homo sapiens

<220>

<221> Artificial sequence

<222> (1)...(20)

<223> Synthetically generated primer

<400> 16

cttcgacgcc ccacactcat

<210> 17  
<211> 20  
<212> DNA  
<213> Homo sapiens

<220>  
<221> Artificial sequence  
<222> (1)...(20)  
<223> Synthetically generated primer

<400> 17  
atgagtgtgg ggcgtcgaag